

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 05:58:15 ; Search time 2251.99 Seconds  
(without alignments)  
12849.734 Million cell updates/sec

Title: US-09-821-839-1  
Perfect score: 2144  
Sequence: 1 actgataagccactctct.....aaaaaaaaaaaaaaaaaaaaa 2144

Scoring table: IDENTITY\_MDC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: em\_estba:\*

- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pln:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609.8	28.4	1233	12	B10183
2	188.8	8.8	192	12	B97951
3	188.8	8.8	818	12	BH530370
4	175	8.2	531	10	BF291837
5	172.6	8.1	1166	12	B12531
6	165.2	7.7	803	12	BH530380
7	152.4	7.1	465	12	BH462012
8	147.4	6.9	727	12	BH487741
9	146.8	5.4	336	12	CNS00MBM
10	96.4	4.5	498	10	BM270448
11	93.2	4.3	612	12	BH477964
12	80.8	3.8	605	12	BH462017
13	70.6	3.3	791	12	AZ686821
14	70.4	3.3	668	9	AL514901
15	68.4	3.2	1225	12	CNS0161D
16	68.4	3.2	1309	10	BE420736
17	68	3.2	1101	12	CNS001FB

18	67.8	3.2	330	9	AL513817	AL513817
19	67.8	3.2	634	9	AL514047	AL514047
20	67.6	3.2	410	9	AL513713	AL513713
21	67.6	3.2	590	9	AL515321	AL515321
22	67.4	3.1	423	9	AM119922	AM119922
23	67.2	3.1	123	12	A0922590	A0922590
24	66.2	3.1	661	12	CNS04QDH	CNS04QDH
25	66.2	3.1	987	12	CNS014PQ	CNS014PQ
26	65.8	3.1	388	12	CNS039K1	CNS039K1
27	65.6	3.1	401	9	AL515191	AL515191
28	65.6	3.1	329	9	AL513719	AL513719
29	65.6	3.1	456	9	AL513813	AL513813
30	65.6	3.1	523	9	AL514015	AL514015
31	65.6	3.1	329	9	AL514935	AL514935
32	65.4	3.1	421	10	AL513719	AL513719
33	65.4	3.1	421	10	BM270739	BM270739
34	65.2	3.0	714	12	A0324694	A0324694
35	65.2	3.0	777	12	CNS025MB	CNS025MB
36	65.2	3.0	988	12	CNS0072R	CNS0072R
37	65	3.0	250	10	BF742555	BF742555
38	64.6	3.0	230	9	AL511812	AL511812
39	64.2	3.0	453	10	BF298095	BF298095
40	64.2	3.0	618	10	BE874847	BE874847
41	64.2	3.0	767	12	CNS008OX	CNS008OX
42	64.2	3.0	951	12	AZ672893	AZ672893
43	64	3.0	954	12	BH162327	BH162327
44	63.8	3.0	279	9	AL540752	AL540752
45	63.8	3.0	633	9	AL513979	AL513979

## ALIGNMENTS

RESULT 1  
B10183/c  
LOCUS B10183  
DEFINITION F19N12-Sp6 TGF Arabidopsis thaliana genomic clone F19N12, DNA sequence.  
ACCESSION B10183  
VERSION B10183.1  
KEYWORDS GI:2091302  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 1233)  
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.  
BAC End Sequences at ATGC  
Unpublished (1997)  
Other\_GSSs: F19N12-77  
Contact: Ecker J.  
Arabidopsis Thaliana Genome Center  
University of Pennsylvania  
Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104  
Tel: 215-898-9384  
Fax: 215-898-8780  
Email: jacker@atgenom.bio.upenn.edu  
Seq primer: Sp6  
Class: BAC ends  
High quality sequence start: 87  
High quality sequence stop: 806.  
Location/Qualifiers  
1. 1233  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="F19N12"  
/clone\_1db="TGF"  
/sex="hermaphrodite"  
/note="Vector: BelobAC11; Site\_1: EcoRI; Site\_2: EcoRI;

